

Figure 1A

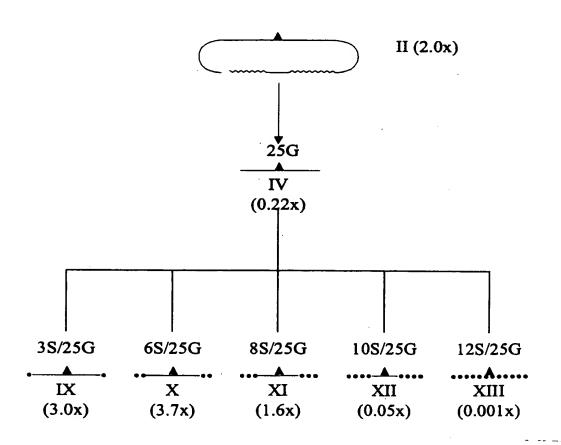
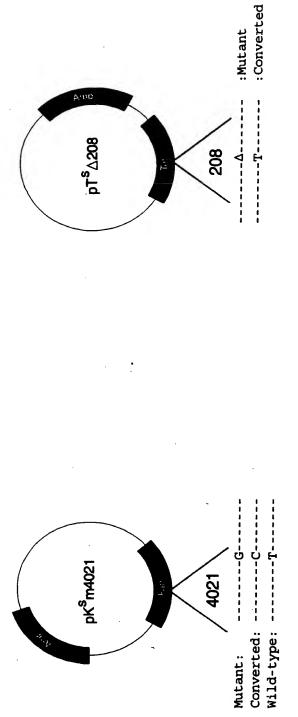


Figure 1B

# Plasmids, DNA targets and chimeric oligonucleotides



KanGG

TGCGCGaaggcugucgTAACgucagugauaT T TCGCGC TTCCCACATCGCCAGTCACTATT 3' 5'

Tet∆208T

Figure 1C

## **DNA SEQUENCE ANALYSES**

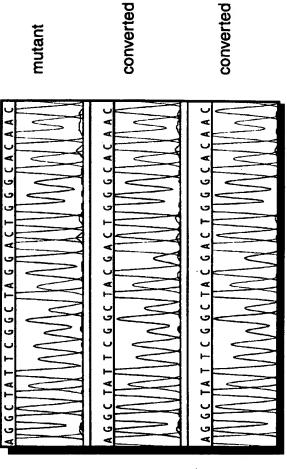


Figure 1D

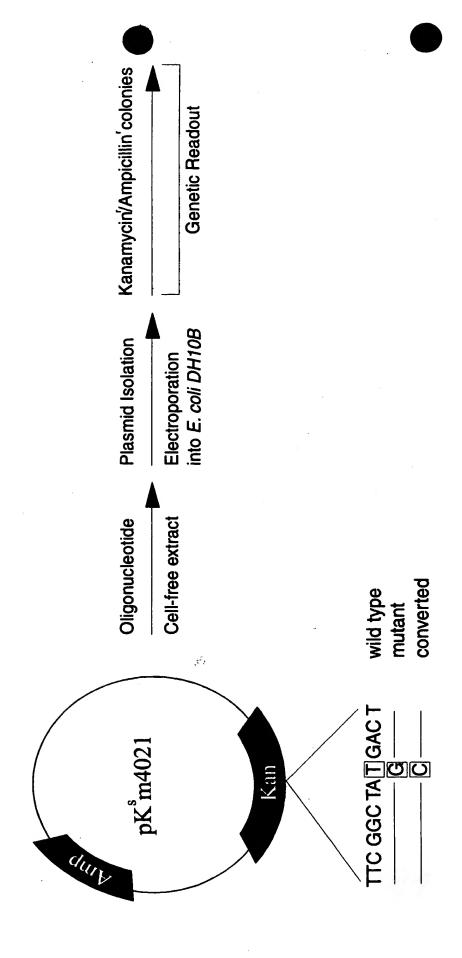
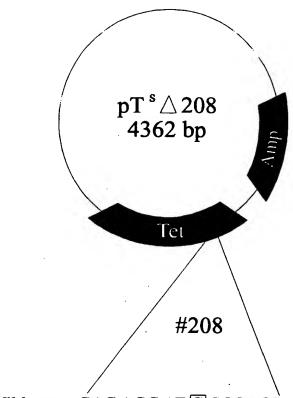


Figure 2



Wild type: GAC AGC AT CGCCAGT Mutant: GAC AGC AT - GCCAGT Converted: GAC AGC AT TGCCAGT

### Sequence analysis of Tet<sup>r</sup> plasmid $\triangle 208$

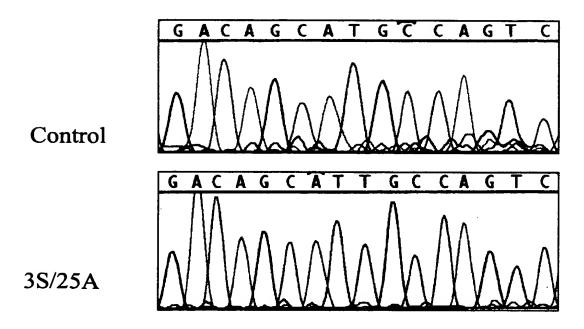
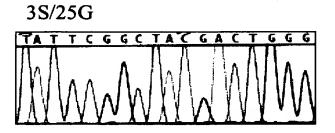
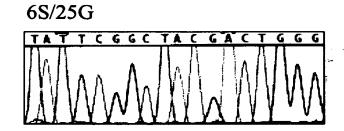


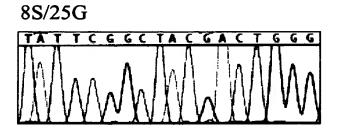
Figure 3

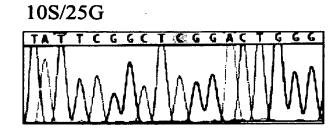
### DNA sequence analysis of Kan<sup>r</sup> plasmids

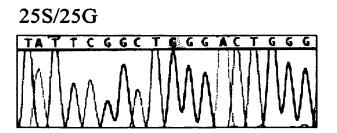
Target codon distribution					
oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)		+			
2) 6S/25G (20)		+			
3) 8S/25G (20)		+			
4) 10S/25G (18)		+		+(2)	+(2)
5) 25S/25G (4)			+(2)	+(2)	

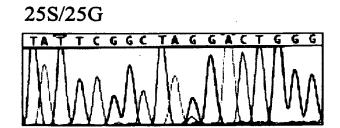












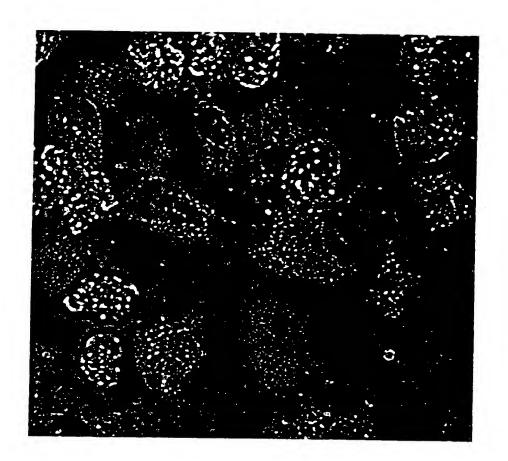


Figure 5

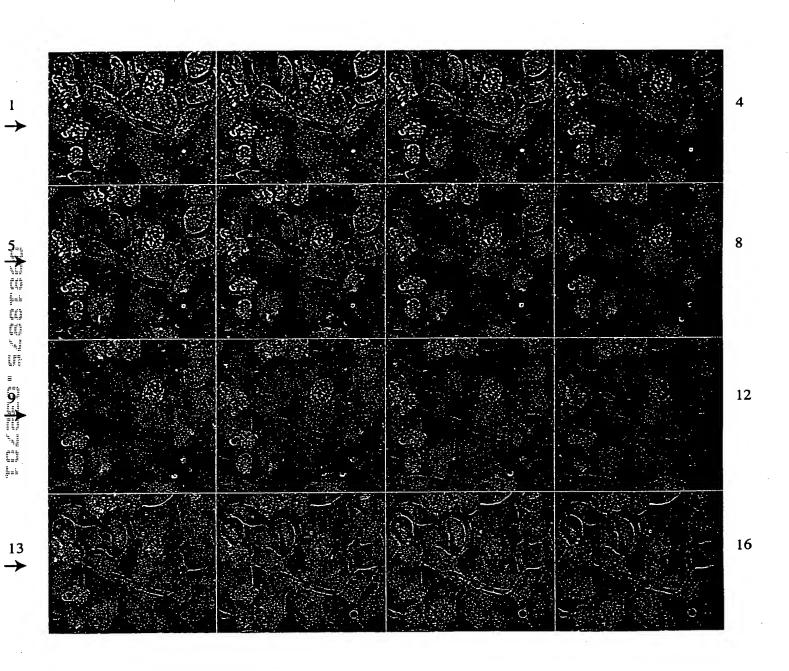


Figure 6

GIGGATAATGICCT Sequence of normal allele: GTGGATATGTCCT Target/existing mutant:

Desired alteration:

GTGGATACGTCCT

### Figure 7A

pAURHYG(x)EGFP

GTGGATACGTCCT Sequence of normal allele: GTGGATATGTCCT GTGGATAGGTCCT Target/existing mutant: Desired alteration:

nintation at position 137 of the hyg coding region Figure

HygE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

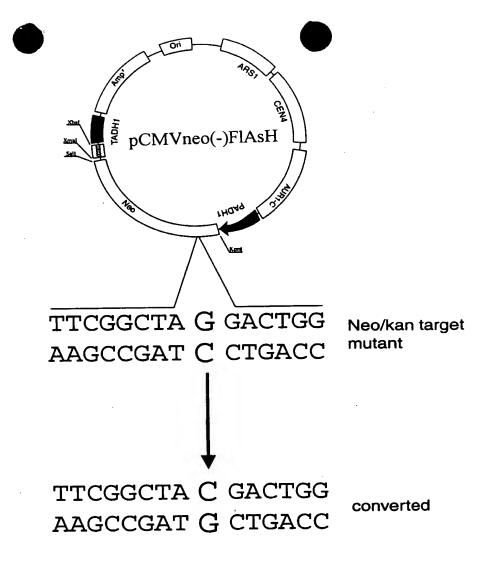
HygE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TCT AC-3'

 $\frac{\text{HygE3T}/74\alpha:}{\text{CAG}}$  5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA GCT GAA AGC ACG  $\frac{\text{AG}}{\text{AG}}$ -3'

### HyqGG/Rev:

Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG A-3'

Figure 8



### **FUSION GENE FOR LIGAND BINDING**

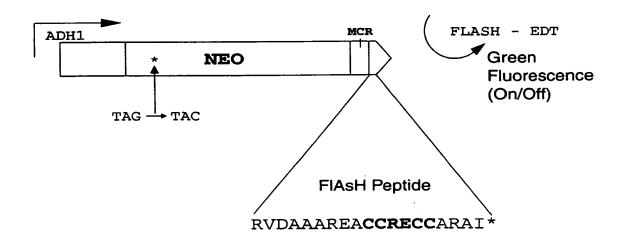


Figure 9

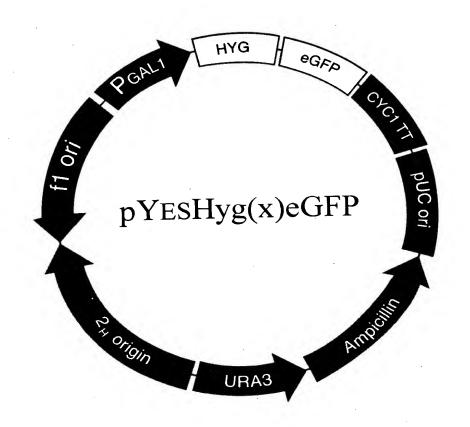


Figure 10